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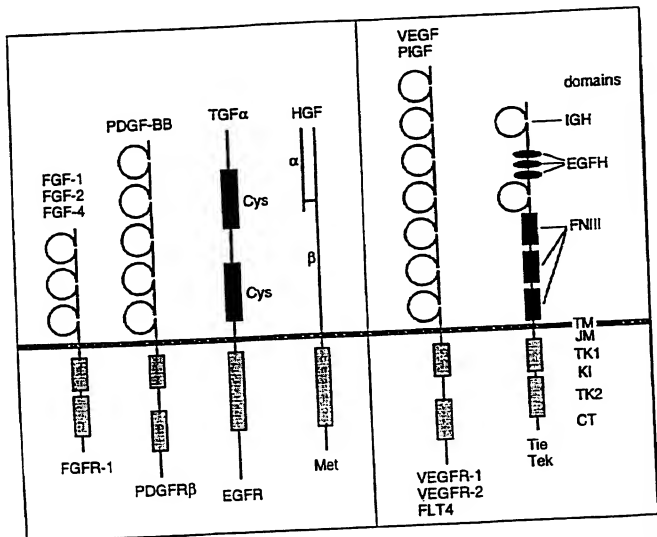


FIGURE 1

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1	50
PDGF-AMRTLACLLL
PDGF-BMNRCA.LFL
PLGF-1
VEGF165
VEGF-B167
VEGF-CAFESGLDSD AEPDAGEATA
51	100
PDGF-A	LGCCYLHVL AEEAIEPREV IERLARSQIH SIRDQLRLE IDSVGSEDSL
PDGF-B	SLCCYLRLVS AEGDPIPEEL YEMLSHSIR SFDDLQRLH GDP.GEEDGA
PLGF-1MPVM RLFP.C..FLQ LLAGIAL... PAVPPQW..
VEGF165M NFLLS..WVH WSLALLLYLH HAKWSQAA..
VEGF-B167M SPLLR..RL LLALLQLAPA QAPVSP...
VEGF-C	YASKDLEQL RSVSSVDELM TVLYPEYWKM YKQRLKGGW QHNREQANLN
101	150
PDGF-A	DTSLRAHGVH ATKHVPEKRP LPIRRKRSI.....EEAVP AVCKTRTVIY
PDGF-B	ELDLNTRSH SGGELES... LARGRSLG SLTIAEPAMI AECKTRTEVF
PLGF-1ALSAG NGSEVEVWP FQE.VVGR... SYCRALERLV
VEGF165PMAEG GGQNHHEVVK FMD.VYQR... SYCHPIETLV
VEGF-B167D APGHQRKVS WID.VYTR... ATCQPREVVV
VEGF-C	SRTETIKFA AAHVNTILK SIDNEWK... TQCMPREVCI
151	200
PDGF-A	EIPRSQVDPT SANFLIWPPC VEVKRTGCC NTSSVKCQPS RVHRSVKVA
PDGF-B	EISRRILDRT NANFLVMPCC VEVQRCGCC NNRNVQCRPT QVQLRPVQVR
PLGF-1	DVSEVPSEV ..EHMFSPCC VSLLRCTGCC GDNELHCVPV ETANVTMLL
VEGF165	DIFQEPDEI ..EYIFKPS VPLMRCGCC NDEGLECVPT EESNITMQIM
VEGF-B167	PLTVELMGTV ..AKQLVPSC VTQRCGCC PDGLEGCVPT GQHQVRMQL
VEGF-C	DVGKEFGVAT ..NTFFKPPC VSVYRCGCC NSEGLQCMNT STSYLSKTLF

FIGURE 2A

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201	PDGF-A	KVEYVRKKPK LKEVQRLEE HLEACAT..	AARPVTRSPG	TSLNPDYREE	250
	PDGF-B	KIEIVRKKPI FKKATVTLED HLAACKETVA	AARPVTRSPG	GSQEQRAKTP	
	PIGF-1	KIRSG..DRP .SYVELTFSQ HVRCECRPLR	
	VEGF165	RIKPH..OGQ .HIGEMSFLQ HNKCECRPKK	DR.....	
	VEGF-B167	MIRVP..SSQ ..LGEMSLEE HSQCECRPKK	KD.....	
	VEGF-C	EITVPLSQGP .KPVITISFAN HTSCRCNSKL	DVYRQVHSII	RRSLPATLPQ	
							300
	PDGF-A	DTDVR.....	
	PDGF-B	QTRVTIRTVR VRRPPKGRHR KFKHTHDKTA	LKETLGA...	
	PIGF-1	
	VEGF165	
	VEGF-B167	
	VEGF-C	COAANKTCPT NYMWNHICR CLAQEDFMFS	SDAGDSDTDG	FHDICGPNKE	
							350
	PDGF-A	
	PDGF-B	
	PIGF-1	
	VEGF165	QDPQTKCSC KNTDS.RCKA ROELNERTC	RCDKPRR...	
	VEGF-B167	PDPTCRRC RRRSFLRCQG RGLNLPDTC	RCKKLRR...	
	VEGF-C	LDEETQCQVC RAGLRPASCG PHKELDRNSC	QCVCKNKLFP	SQCGANREFD	

FIGURE 2 B

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	351		400
PDGF-A
PDGF-B
PlGF-1
VEGF165
VEGF-B167
VEGF-C	ENTCQCVCCKR TCPRNQPLNP GKCAECTES POKCLLKGGK FHHQTCSYR		
	401		434
PDGF-A
PDGF-B
PlGF-1
VEGF165
VEGF-B167
VEGF-C	RPCTNRQKAC EPGFSYSEEV CRCVPSYWKR PQMS		

FIGURE 2 C

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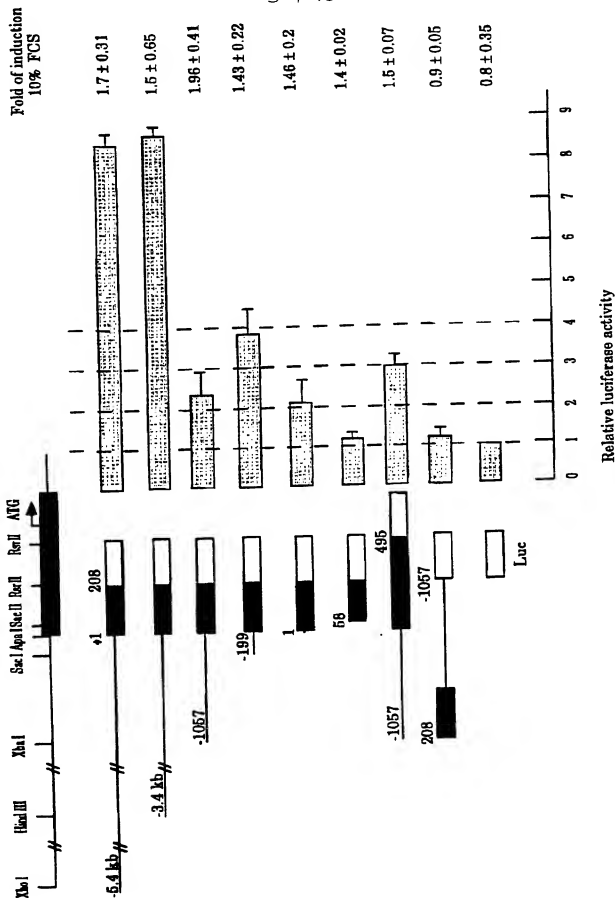


FIGURE 3

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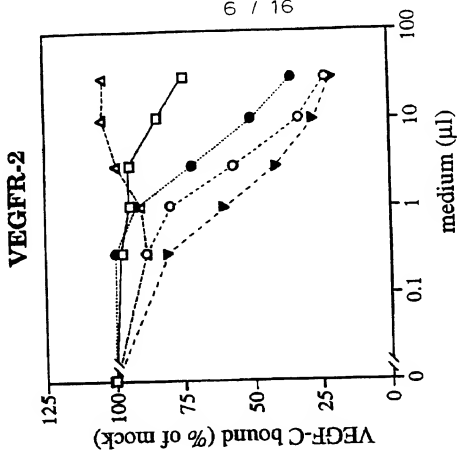


FIGURE 4B

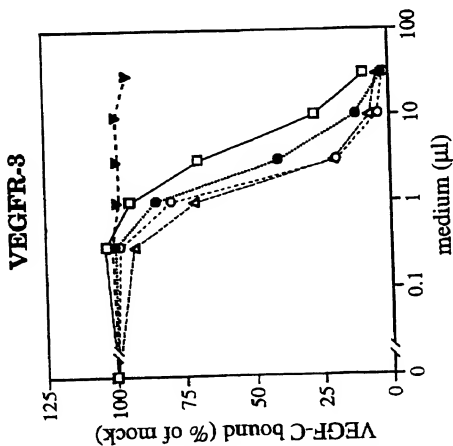


FIGURE 4A

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VEGF-C alignment

						50
Hum	1	HMLLGFFSVA	CSLLAAALIP	GPREAPAAAA	AFESGLDLSA	AEPDAGEATA
Mou		MHLLCFLSLA	CSLLAAALIP	SPREAPATVA	AFESGLGFSE	AEPDGGEVKA
Qua		MHLLLEMLSLG	CCLAAGAVLL	GPRQPPVA.A	AYESGHGYIE	EPPGAGEPKA
	51					100
Hum		YASKDLEEQL	RSVSSVDELM	TVLYPEYWKM	YKQCLRKGW	QHNREQANLN
Mou		FEGKDLLEQL	RSVSSVDELM	SVLYPDYWKM	YKQCLRKGW	Q....OPTLN
Qua		HASKDLEEQL	RSVSSVDELM	TVLYPEYWKM	FKQCLRKGW	QHNREHSSD
	101					150
Hum		SRTTEETIKFA	AAHYNTEILK	SIDNEWRTQ	CMPREVCIDV	GKEFGVATNT
Mou		TRTGDSVKFA	AAHYNTEILK	SIDNEWRTQ	CMPREVCIDV	GKEFGAATNT
Qua		TRSDDSLKFA	AAHYNAEILK	SIDTEWRKTQ	GMPREVCVDL	GKEFGATTNT
	151					200
Hum		FFKPPCVSVY	RCGGCCNSEG	LQCMNTSTSY	LSKTLFEITV	PLSQGPKPVT
Mou		FFKPPCVSVY	RCGGCCNSEG	LQCMNTSTGY	LSKTLFEITV	PLSQGPKPVT
Qua		FFKPPCVSIY	RCGGCCNSEG	LQCMNISTNY	ISKTLFEITV	PLSHGPKPVT
	201					250
Hum		ISFANETSCR	CMSKLDVYRQ	VHSIIRRLP	ATLPQCCAAN	KTCPTNYMWN
Mou		ISFANETSCR	CMSKLDVYRQ	VHSIIRRLP	ATLPQCCAAN	KTCPTNYMWN
Qua		VSFANETSCR	CMSKLDVYRQ	VHSIIRRLP	ATQTQCHVAN	KTCPKNHVWN
	251					300
Hum		NHICRCLAQE	DFMFSSDAGD	DSTDGFHDIC	GPKNELDEET	CQCVCRCAGLR
Mou		NYMCRCLAQO	DFIFYSNVED	DSTNGFHDVC	GPKNELDEET	CQCVCCKGGLR
Qua		NQICRCLAQH	DFGFSSHLGD	SDTSEGPHIC	GPKNELDEET	CQCVCCKGGVR
	301					350
Hum		PASCGPHKEL	DRNSCQCVCCK	NKLFPSQCGA	NREFDENTCQ	CVCKRTCPRN
Mou		PSCGPHKEL	DRNSCQCVCCK	NKLFPSQCGA	NREFDENTCQ	CVCKRTCPRN
Qua		PISCGPHKEL	DRASCQCVCCK	NKLLPSSCGP	NKEFDEEKQ	CVCKKTCPKH
	351					400
Hum		QPLNPGKAC	ECTESPQKCL	LKGKKFFHHQT	CSCYRRPCTN	RQKACEPGFS
Mou		QPLNPGKAC	ECTENTQKCF	LKGKKFFHHQT	CSCYRRPCAN	RLKHCDPGLS
Qua		HPLNPAKIC	ECTESPKNCF	LKGKRFHHQT	CSCYRRPCTV	RTKRCDAAGFL
	401					420
Hum		YSEEVCRCPV	SYWKRPFQMS*			
Mou		FSEEVCRCPV	SYWKRPHLN.			
Qua		LAEEVCRCPV	TSWKRPLMN*			

FIGURE 5

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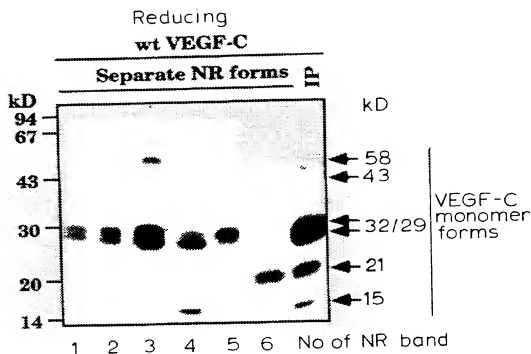


FIGURE 6A

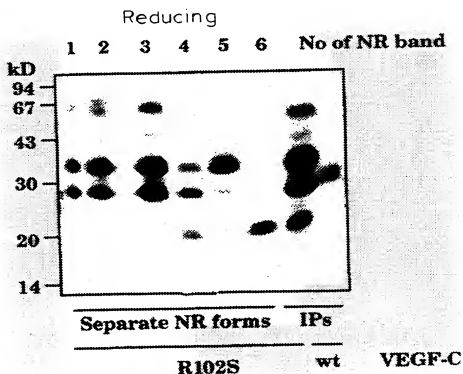


FIGURE 6C

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Non-reducing

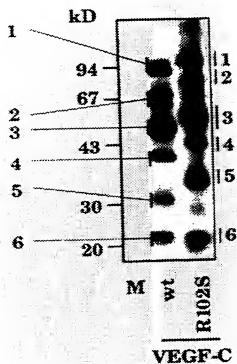


FIGURE 6B

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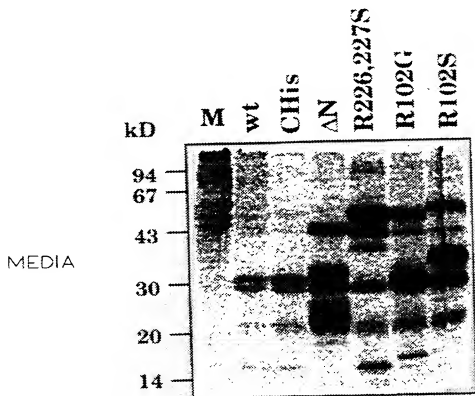


FIGURE 7A

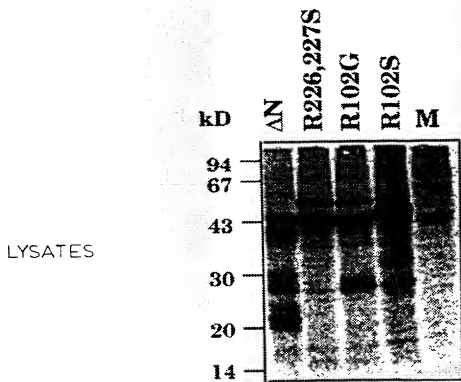


FIGURE 7B

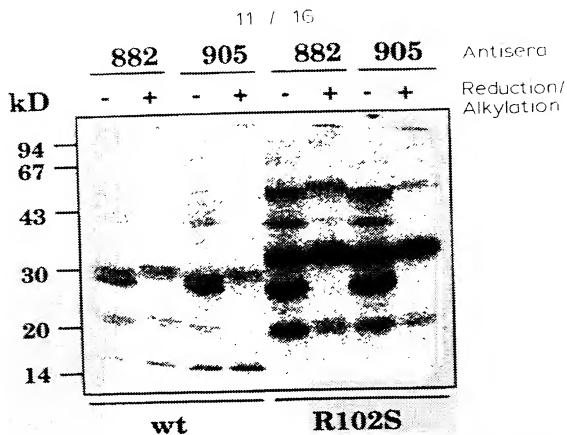


FIGURE 8A

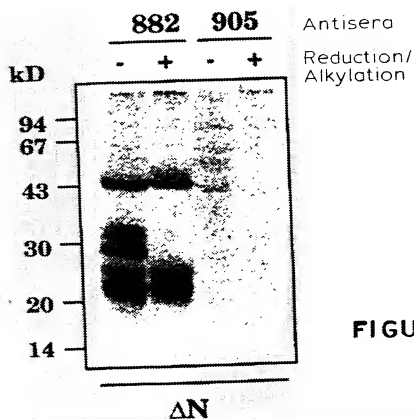


FIGURE 8B

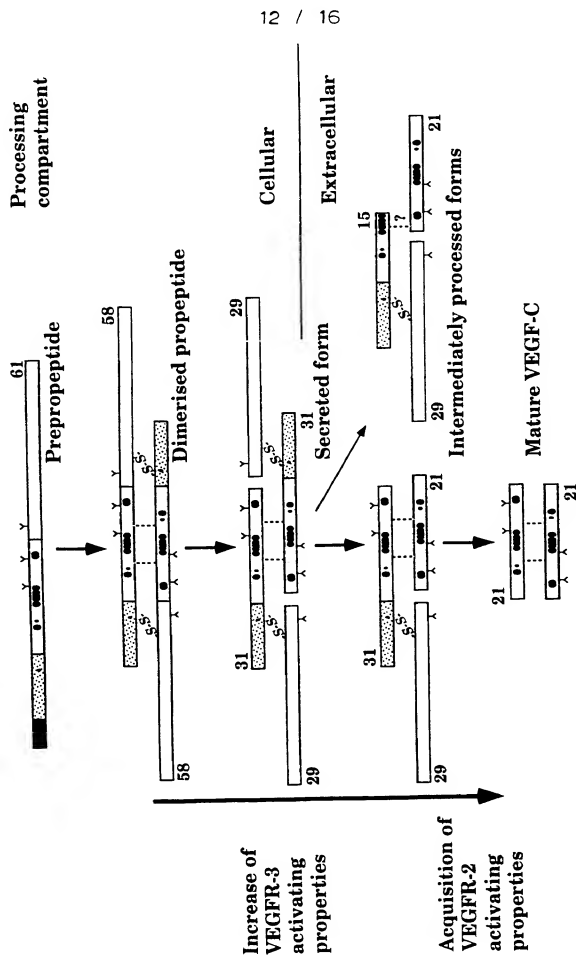


FIGURE 9

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HUMAN Exon length	Donor site	Intron length	Acceptor site
.....	G...E...A...T(49)	A...Y...A...S.
E1.....	GGC.GAG.GCC.ACG.gtaggtctgcgt...	>10.kb.	TTTCTTTGACAG.GCT.TAT.GCA.AGC
.....	E...I...L...K(116)	S...I...D...N.
E2.214.bp.	GAG.ATC.TTG.AAA.Agtaagtatggg...	1.6.kb.	atgacttgacagGT.ATT.GAT.AAT
.....	L...S...K...T(180)	L...F...E...I.
E3.191.bp.	CTC.AGC.AAG.ACG.gtggtattgt...	9.kb.	cccttctttag.TTA.TTT.GAA.ATT
.....	T...L...P...Q(231)	C...Q...A...A.
E4.152.bp.	ACA.CTA.CCA.CAGtgagtatgaattaaa...	>10.kb.	ttcttccaaagG.TGT.CAG.GCA.GCG
.....	A...G...D... (266)	D...S...T...D.
E5.107.bp.	GCT.GGA.GAT.Ggtagcagaatg.....	301.bp.	ctatttgtctagAC.TCA.ACA.GAT
.....	Q...T...C...S(378)	C...Y...R...R.
E6.334.bp.	CAA.ACA.TGC.AGtaagagatcc.....	>10.kb.	tgttctcctagC.TGT.TAC.AGA.CGG
.....	Q...M...S(419) Stop	
E7.(501).bp.	CAA.ATG.AGC.TAA.GTATGTACTGTT...ATTGTATTAT		

FIGURE 11A

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MOUSE Exon length	Donor site	Intron length	Acceptor site
.....G...E...V...K(49).....G...E...V...K(49).....A...F...E...G.A...F...E...G.
E1.....GGC.GAG.GTC.AAG.gtaggtgaagg.>10.kb.attgtctttgacag.GCT.TTT.TGA.AGGGGC.GAG.GTC.AAG.gtaggtgaagg.>10.kb.attgtctttgacag.GCT.TTT.TGA.AGGGCT.TTT.TGA.AGGGCT.TTT.TGA.AGG
.....E...I...L...K(116).....E...I...L...K(116).....S...I...D...N.S...I...D...N.
E2.201.bp..GAG.ATC.CTG.AAA.Agtaagtag.....4.kb...tgtgactcgacagGT.ATT.GAT.AATGAG.ATC.CTG.AAA.Agtaagtag.....4.kb...tgtgactcgacagGT.ATT.GAT.AATL...F...E...I.L...F...E...I.
.....L...S...K...T(180).....L...S...K...T(180).....L...F...E...I.L...F...E...I.
E3.191.bp..CTC.AGC.AAG.ACG.gtaggtat.....9.kb..ttgtccctttag.TTG.TTT.GAA.ATTCTC.AGC.AAG.ACG.gtaggtat.....9.kb..ttgtccctttag.TTG.TTT.GAA.ATTC...Q...A...A.C...Q...A...A.
.....T...L...P...Q(231).....T...L...P...Q(231).....C...Q...A...A.C...Q...A...A.
E4.152.bp..ACA.TTA.CCA.CAgtagtagt.....10.kb.gtcccccaaaagG.TGT.CAG.GCA.GCTACA.TTA.CCA.CAgtagtagt.....10.kb.gtcccccaaaagG.TGT.CAG.GCA.GCTD...S...T...N.D...S...T...N.
.....N...V...E...D(266).....N...V...E...D(266).....D...S...T...N.D...S...T...N.
E5.107.bp..AAT.GTT.GAA.GAT.Ggtaagtaaaa...350.bp.....tctagAC.TCA.ACC.AATAAT.GTT.GAA.GAT.Ggtaagtaaaa...350.bp.....tctagAC.TCA.ACC.AATC...Y...R...R.C...Y...R...R.
.....Q...T...C...S(378).....Q...T...C...S(378).....C...Y...R...R.C...Y...R...R.
E6.334.bp..CAA.ACA.TGC.AGgtaaggagtgt.....6.kb..ttttcccttagT.TGT.TAC.AGA.AGACAA.ACA.TGC.AGgtaaggagtgt.....6.kb..ttttcccttagT.TGT.TAC.AGA.AGApolyA.....polyA.....
.....H...L...N(415)Stop.....H...L...N(415)Stop.....polyA.....polyA.....
E7.506.bp..CAT.CTG.AAC.TAA.GATCATACC...ATTGTATTATATAgctgtgaagCAT.CTG.AAC.TAA.GATCATACC...ATTGTATTATATAgctgtgaagpolyA.....polyA.....

FIGURE 11B

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Schematic structure of the human VEGF-C gene

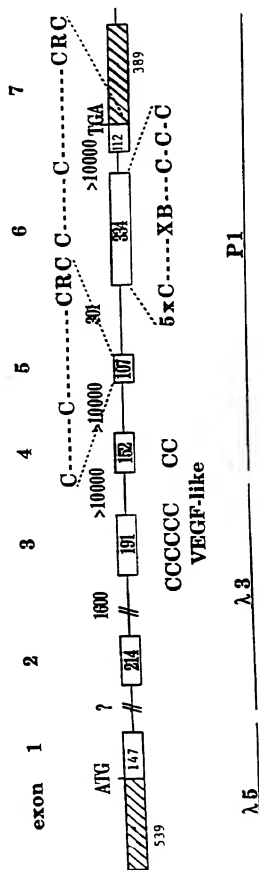


FIGURE 12